

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 21:57:27 ; Search time 9811 Seconds
(without alignments)
10989.232 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattataacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1684.4	99.9	1740	2 BD093391	BD093391 Method fo
2	1684.4	99.9	1740	5 AB006590	AB006590 Homo sapi
3	1683.4	99.8	2011	2 AR606192	AR606192 Sequence
4	1683.4	99.8	2011	2 AX234658	AX234658 Sequence
5	1683.4	99.8	2011	2 AX676912	AX676912 Sequence
6	1683.4	99.8	2011	5 AF051427	AF051427 Homo sapi
7	1667.4	98.9	1898	2 A65127	A65127 Sequence 24

	8	1667.4	98.9	1898	2	AR454163	AR454163 Sequence
	9	1667.4	98.9	1898	2	AR490594	AR490594 Sequence
	10	1667.4	98.9	1898	2	AX323078	AX323078 Sequence
	11	1637.4	97.1	2433	2	BD170497	BD170497 Fluoresce
	12	1634	96.9	1647	2	BD091391	BD091391 Estrogen
	13	1634	96.9	1647	2	AR233984	AR233984 Sequence
	14	1634	96.9	1647	2	AR316860	AR316860 Sequence
	15	1634	96.9	1647	2	AX029400	AX029400 Sequence
	16	1609.4	95.5	1660	2	AX592833	AX592833 Sequence
c	17	1609.4	95.5	1660	2	AX592834	AX592834 Sequence
	18	1496.4	88.8	2041	5	AF051428	AF051428 Homo sapi
	19	1496.4	88.8	2745	5	AF060555	AF060555 Homo sapi
	20	1495.8	88.7	3593	5	AB006589	AB006589 Homo sapi
	21	1485.6	88.1	1651	5	CJERB	Y09372 C.jacchus m
	22	1453.6	86.2	1460	2	A61586	A61586 Sequence 4
	23	1453.6	86.2	1460	2	AR075921	AR075921 Sequence
	24	1453.6	86.2	1460	2	BD131061	BD131061 Orphan re
	25	1453.6	86.2	1460	2	AX022458	AX022458 Sequence
	26	1450.4	86.0	1460	2	BD078109	BD078109 Discrimin
	27	1450	86.0	1560	5	HSRNAERB	X99101 H.sapiens m
	28	1434	85.1	1434	2	A65104	A65104 Sequence 1
	29	1434	85.1	1434	2	AR454145	AR454145 Sequence
	30	1434	85.1	1434	2	AR490576	AR490576 Sequence
	31	1434	85.1	1434	2	AX323055	AX323055 Sequence
	32	1405.2	83.3	5554	5	AB209620	AB209620 Homo sapi
	33	1374.2	81.5	1640	5	AF393815	AF393815 Macaca ar
	34	1306.6	77.5	1566	5	AF393816	AF393816 Callithri
	35	1256.6	74.5	1611	14	AF110402	AF110402 Bos tauru
	36	1254.6	74.4	1584	14	AF177936	AF177936 Ovis arie
	37	1247.2	74.0	2344	6	AB190769	AB190769 Rattus no
	38	1247	74.0	1251	2	A65105	A65105 Sequence 2
	39	1247	74.0	1251	2	AR454146	AR454146 Sequence
	40	1247	74.0	1251	2	AR490577	AR490577 Sequence
	41	1247	74.0	1251	2	AX323056	AX323056 Sequence
	42	1247	74.0	1257	2	A65123	A65123 Sequence 20
	43	1247	74.0	1257	2	AR454160	AR454160 Sequence
	44	1247	74.0	1257	2	AR490591	AR490591 Sequence
	45	1247	74.0	1257	2	AX323074	AX323074 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:28:57 ; Search time 341 Seconds
(without alignments)
9251.289 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattataacttgccac.....agaaccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1684.4	99.9	1745	3	US-09-949-016-1563	Sequence 1563, Ap
2	1683.4	99.8	2011	3	US-09-768-185A-2	Sequence 2, Appli
3	1667.4	98.9	1898	3	US-09-608-088-24	Sequence 24, Appl
4	1667.4	98.9	1898	3	US-09-711-288-24	Sequence 24, Appl
5	1634	96.9	1647	3	US-09-139-617-2	Sequence 2, Appli
6	1634	96.9	1647	3	US-09-561-741A-2	Sequence 2, Appli
7	1634	96.9	1647	3	US-09-558-795-2	Sequence 2, Appli
8	1453.6	86.2	1460	2	US-08-836-620A-4	Sequence 4, Appli
9	1434	85.1	1434	3	US-09-608-088-1	Sequence 1, Appli
10	1434	85.1	1434	3	US-09-711-288-1	Sequence 1, Appli
11	1247	74.0	1251	3	US-09-608-088-2	Sequence 2, Appli
12	1247	74.0	1251	3	US-09-711-288-2	Sequence 2, Appli

13	1247	74.0	1257	3	US-09-608-088-20	Sequence 20, Appl
14	1247	74.0	1257	3	US-09-711-288-20	Sequence 20, Appl
15	1233.6	73.2	2568	2	US-08-836-620A-1	Sequence 1, Appli
16	1099.6	65.2	1458	2	US-08-836-620A-6	Sequence 6, Appli
17	453.4	26.9	68452	3	US-09-949-016-13305	Sequence 13305, A
18	453.4	26.9	325791	3	US-09-768-185A-1	Sequence 1, Appli
19	395.8	23.5	2764	3	US-09-893-666A-1	Sequence 1, Appli
20	390.8	23.2	4963	2	US-08-076-726-16	Sequence 16, Appl
21	390.8	23.2	4963	2	US-08-260-452-9	Sequence 9, Appli
22	390.8	23.2	4963	2	US-08-481-970-9	Sequence 9, Appli
23	390.8	23.2	4963	2	US-08-897-719-9	Sequence 9, Appli
24	390.8	23.2	4963	3	US-09-163-269-9	Sequence 9, Appli
25	390.8	23.2	4963	3	US-09-281-674-9	Sequence 9, Appli
26	390.8	23.2	4963	3	US-09-777-317B-9	Sequence 9, Appli
27	389.2	23.1	2092	3	US-10-052-092-6	Sequence 6, Appli
28	389.2	23.1	6450	3	US-09-041-886-34	Sequence 34, Appl
29	389.2	23.1	6450	3	US-08-453-998-1	Sequence 1, Appli
30	389.2	23.1	6450	3	US-10-027-983-3	Sequence 3, Appli
31	389.2	23.1	6450	3	US-09-949-016-18	Sequence 18, Appl
32	389.2	23.1	6450	3	US-10-052-092-1	Sequence 1, Appli
33	389.2	23.1	6450	3	US-10-052-092-7	Sequence 7, Appli
34	389.2	23.1	6450	3	US-10-081-563-1	Sequence 1, Appli
35	389.2	23.1	6610	3	US-10-052-092-20	Sequence 20, Appl
36	388	23.0	1788	3	US-10-052-092-24	Sequence 24, Appl
37	366.2	21.7	1978	3	US-10-052-092-23	Sequence 23, Appl
38	326.6	19.4	2106	3	US-10-052-092-5	Sequence 5, Appli
39	312.4	18.5	8566	3	US-10-027-983-10	Sequence 10, Appl
40	296.4	17.6	2495	3	US-09-771-357-104	Sequence 104, App
41	296.4	17.6	2495	3	US-10-059-579A-104	Sequence 104, App
42	287.2	17.0	1218	3	US-10-027-983-98	Sequence 98, Appl
43	285.6	16.9	1644	3	US-10-052-092-2	Sequence 2, Appli
44	285.6	16.9	1956	3	US-08-693-940-2	Sequence 2, Appli
45	285.6	16.9	1956	3	US-09-566-660-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:59:46 ; Search time 2247 Seconds
(without alignments)
9219.828 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattataacttgcccac.....agaaccacagtcctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1686	100.0	1686	9	US-10-745-379-1 Sequence 1, Appli
2	1686	100.0	1686	16	US-11-026-800-1 Sequence 1, Appli
3	1684.4	99.9	1740	3	US-09-815-068A-1 Sequence 1, Appli
4	1684.4	99.9	1740	6	US-10-198-785-1 Sequence 1, Appli
5	1683.4	99.8	2011	4	US-09-768-185A-2 Sequence 2, Appli
6	1683.4	99.8	2011	6	US-10-157-031-105 Sequence 105, App

7	1683.4	99.8	2011	7	US-10-392-274-3	Sequence 3, Appli
8	1683.4	99.8	2011	10	US-10-888-313A-101	Sequence 101, App
9	1683.4	99.8	6777	7	US-10-376-566-10	Sequence 10, Appl
10	1637.4	97.1	2433	8	US-10-460-845-1	Sequence 1, Appli
11	1496.4	88.8	2041	10	US-10-756-149-1507	Sequence 1507, Ap
12	1496.4	88.8	2745	11	US-10-826-585-22	Sequence 22, Appl
13	1495.8	88.7	3593	7	US-10-376-566-3	Sequence 3, Appli
14	1453.6	86.2	1460	6	US-10-278-481-4	Sequence 4, Appli
15	1433.8	85.0	1682	7	US-10-373-271-2	Sequence 2, Appli
16	1236.4	73.3	2555	16	US-11-136-527-2114	Sequence 2114, Ap
17	1233.6	73.2	2568	6	US-10-278-481-1	Sequence 1, Appli
18	1167.4	69.2	1427	7	US-10-376-566-15	Sequence 15, Appl
19	1099.6	65.2	1458	6	US-10-278-481-6	Sequence 6, Appli
20	1056.4	62.7	1512	16	US-11-136-527-3577	Sequence 3577, Ap
21	865	51.3	1215	7	US-10-376-566-14	Sequence 14, Appl
22	600	35.6	600	13	US-11-060-756-2172	Sequence 2172, Ap
23	600	35.6	600	13	US-11-060-756-2173	Sequence 2173, Ap
24	600	35.6	600	13	US-11-060-756-6444	Sequence 6444, Ap
25	600	35.6	600	13	US-11-060-756-6445	Sequence 6445, Ap
26	453.4	26.9	113000	7	US-10-376-566-16	Sequence 16, Appl
27	453.4	26.9	325791	4	US-09-768-185A-1	Sequence 1, Appli
28	452.4	26.8	597	3	US-09-864-761-7903	Sequence 7903, Ap
29	433.8	25.7	2384	8	US-10-663-561-148	Sequence 148, App
30	415.8	24.7	2188	8	US-10-663-561-147	Sequence 147, App
31	396.8	23.5	600	16	US-11-136-527-7673	Sequence 7673, Ap
32	395.8	23.5	2764	3	US-09-893-666A-1	Sequence 1, Appli
33	391.2	23.2	2043	8	US-10-663-561-146	Sequence 146, App
34	390.8	23.2	1788	3	US-09-853-033-1	Sequence 1, Appli
35	390.8	23.2	4963	3	US-09-281-674-9	Sequence 9, Appli
36	390.8	23.2	4963	3	US-09-777-317-9	Sequence 9, Appli
37	390.8	23.2	4963	3	US-09-892-227-9	Sequence 9, Appli
38	389.2	23.1	1785	7	US-10-095-373A-1	Sequence 1, Appli
39	389.2	23.1	1793	13	US-11-035-623-1	Sequence 1, Appli
40	389.2	23.1	1809	13	US-11-035-623-11	Sequence 11, Appl
41	389.2	23.1	2092	3	US-09-952-680A-9	Sequence 9, Appli
42	389.2	23.1	2092	6	US-10-052-092-6	Sequence 6, Appli
43	389.2	23.1	2092	7	US-10-157-899A-54	Sequence 54, Appl
44	389.2	23.1	2092	7	US-10-437-107-6	Sequence 6, Appli
45	389.2	23.1	2092	9	US-10-215-982-9	Sequence 9, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 03:22:02 ; Search time 563 Seconds
(without alignments)
4755.765 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattataacttgccac.....agaaccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1683.4	99.8		2011	8	US-11-283-329-93	Sequence 93, Appl
2	1683.4	99.8		2011	9	US-11-346-759-101	Sequence 101, App
3	1000	59.3		1000	8	US-11-266-748A-395231	Sequence 395231,
c 4	1000	59.3		1000	8	US-11-266-748A-466277	Sequence 466277,
5	450.4	26.7		2186	6	US-10-501-227-24	Sequence 24, Appl
6	389.8	23.1		1824	6	US-10-501-227-5	Sequence 5, Appli
7	389.8	23.1		3499	6	US-10-501-227-2	Sequence 2, Appli
8	389.2	23.1		6450	8	US-11-289-102-120	Sequence 120, App
9	389.2	23.1		6450	8	US-11-283-329-91	Sequence 91, Appl
10	389.2	23.1		6450	9	US-11-346-759-100	Sequence 100, App
11	352.8	20.9		963	6	US-10-501-227-25	Sequence 25, Appl
12	319.2	18.9		996	6	US-10-501-227-3	Sequence 3, Appli

	13	179.6	10.7	611	8	US-11-266-748A-214650	Sequence 214650,
c	14	130	7.7	3540	8	US-11-266-748A-71864	Sequence 71864, A
c	15	130	7.7	3540	8	US-11-266-748A-106889	Sequence 106889,
	16	130	7.7	3540	8	US-11-266-748A-124675	Sequence 124675,
	17	129	7.7	1566	6	US-10-526-940-2	Sequence 2, Appli
	18	129	7.7	2221	8	US-11-283-329-95	Sequence 95, Appl
	19	129	7.7	2402	8	US-11-266-748A-32133	Sequence 32133, A
	20	113.8	6.7	1377	6	US-10-526-940-1	Sequence 1, Appli
	21	113.8	6.7	5216	6	US-10-507-700-5	Sequence 5, Appli
	22	113.8	6.7	5253	8	US-11-283-329-99	Sequence 99, Appl
	23	112.2	6.7	1503	6	US-10-526-940-7	Sequence 7, Appli
	24	110.6	6.6	2193	8	US-11-283-329-97	Sequence 97, Appl
	25	105.8	6.3	5221	6	US-10-507-700-3	Sequence 3, Appli
	26	95.2	5.6	3514	6	US-10-523-899-4	Sequence 4, Appli
	27	95.2	5.6	3768	6	US-10-523-899-1	Sequence 1, Appli
	28	95.2	5.6	4314	8	US-11-283-329-107	Sequence 107, App
	29	89.6	5.3	2575	9	US-11-207-382-11	Sequence 11, Appl
	30	88.6	5.3	2263	8	US-11-266-748A-185290	Sequence 185290,
	31	88.6	5.3	2263	8	US-11-266-748A-192812	Sequence 192812,
	32	88.6	5.3	2481	8	US-11-266-748A-59173	Sequence 59173, A
	33	88.6	5.3	2549	8	US-11-283-329-111	Sequence 111, App
	34	88.6	5.3	2699	8	US-11-283-329-109	Sequence 109, App
c	35	88.4	5.2	1442	8	US-11-266-748A-227525	Sequence 227525,
	36	88.4	5.2	1442	8	US-11-266-748A-241597	Sequence 241597,
	37	88.2	5.2	1855	8	US-11-266-748A-27269	Sequence 27269, A
	38	88.2	5.2	2202	8	US-11-283-329-75	Sequence 75, Appl
	39	88	5.2	1000	8	US-11-266-748A-391580	Sequence 391580,
c	40	88	5.2	1000	8	US-11-266-748A-482298	Sequence 482298,
c	41	86.4	5.1	788	8	US-11-266-748A-255985	Sequence 255985,
	42	86.4	5.1	788	8	US-11-266-748A-316502	Sequence 316502,
	43	86.4	5.1	3791	8	US-11-266-748A-32110	Sequence 32110, A
	44	86.4	5.1	3791	9	US-11-207-382-26	Sequence 26, Appl
	45	86.4	5.1	4788	8	US-11-283-329-101	Sequence 101, App

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 22:16:02 ; Search time 8466 Seconds
(without alignments)
11136.309 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattataacttgcccac.....agaaccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
1	1168.4	69.3	2712	6	AK054290	AK054290 Mus muscu
2	1168.4	69.3	3363	6	AK054413	AK054413 Mus muscu
3	962	57.1	3144	6	AK054301	AK054301 Mus muscu
4	584.4	34.7	587	8	CV024245	CV024245 1485 Full
5	500.8	29.7	727	2	BG722442	BG722442 602693671
6	403.4	23.9	621	9	DB025815	DB025815 DB025815
7	364.6	21.6	4248	6	AK041525	AK041525 Mus muscu
8	364.6	21.6	4321	6	AK036627	AK036627 Mus muscu

	9	353.8	21.0	570	9	DB052117	DB052117	DB052117
	10	353.6	21.0	2591	6	AK077236	AK077236	Mus muscu
	11	353.4	21.0	572	9	DB029843	DB029843	DB029843
c	12	288.2	17.1	835	13	CW720839	CW720839	MARC_1130
	13	286.8	17.0	5439	6	HSM807087	BX640939	Homo sapi
	14	278	16.5	4315	6	AK087638	AK087638	Mus muscu
	15	276.6	16.4	703	4	BY720348	BY720348	BY720348
	16	276.6	16.4	873	8	CO808332	CO808332	AGENCOURT
	17	275.2	16.3	675	5	CF913882	CF913882	B0955G07-
c	18	260	15.4	810	13	CW720841	CW720841	MARC_1130
	19	238.6	14.2	375	5	CJ075881	CJ075881	CJ075881
	20	237.8	14.1	387	9	DR000137	DR000137	TC119215
	21	220.2	13.1	663	4	BY720287	BY720287	BY720287
	22	220	13.0	814	13	CW720570	CW720570	MARC_1129
	23	219.6	13.0	1020	6	AK136228	AK136228	Mus muscu
	24	215.8	12.8	735	12	BZ834605	BZ834605	CH240_209
c	25	214	12.7	1160	5	CD508522	CD508522	CDA91-C11
c	26	208	12.3	627	3	BM942391	BM942391	UI-M-BH3-
	27	201.2	11.9	2735	6	AK054182	AK054182	Mus muscu
	28	196.4	11.6	652	7	BB666338	BB666338	BB666338
	29	189.4	11.2	623	9	DN424563	DN424563	LIB4216-1
	30	185.4	11.0	666	7	BB609187	BB609187	BB609187
	31	184.6	10.9	627	7	BB666608	BB666608	BB666608
	32	179.6	10.7	611	4	BX489897	BX489897	DKFZp686N
	33	174.2	10.3	766	13	CW720571	CW720571	MARC_1129
c	34	173.4	10.3	531	1	AA224131	AA224131	zr14e02.r
	35	169.8	10.1	1419	10	DT949269	DT949269	CFW102-E0
c	36	162.4	9.6	528	3	BM933826	BM933826	UI-M-BH3-
	37	162.2	9.6	580	2	BG738138	BG738138	fp04f05.y
	38	157.2	9.3	936	14	DQ038302	DQ038302	Pan trogl
	39	157	9.3	642	7	BF058527	BF058527	7k31h08.x
	40	157	9.3	782	7	AW134052	AW134052	fil14h07.y
	41	157	9.3	1017	14	DQ038301	DQ038301	Homo sapi
	42	155.6	9.2	877	10	DT235626	DT235626	JGI_CAAT8
	43	155.4	9.2	641	7	AW976636	AW976636	EST388745
	44	155	9.2	650	5	CD594261	CD594261	RK090A3F1
	45	155	9.2	650	5	CD594319	CD594319	RK090A4F1